SEQUENCE LISTING

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<150> <151>				3											
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<210> <211> <212> <213>	1 1008 DNA Homo	sapi	ens												
<220> <223>	Inven	itor:	0h i	shi,	Tak	ahid	e; K	oizu	mi,	Tomo	nobu				
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ctc at Leu II	c att e lle	gct Ala 20	act Thr	aac Asn	aca Thr	cta Leu	gtg Val 25	gct Ala	gtg Val	gct Ala	gtg Val	ctg Leu 30	ctg Leu	ttg Leu	96
atc ca lle Hi	c aag s Lys 35	aat Asn	gat Asp	ggt Gly	gtc Val	agt Ser 40	ctc Leu	tgc Cys	ttc Phe	acc Thr	ttg Leu 45	aat Asn	ctg Leu	gct Ala	144
gtg gc Val Al 5	t gac a Asp O	acc Thr	ttg Leu	att Ile	ggt Gly 55	gtg Val	gcc Ala	atc lle	tct Ser	ggc Gly 60	cta Leu	ctc Leu	aca Thr	gac Asp	192
cag ct	c tcc	agc	cct	tct	cgg	ccc	aca	cag	aag	acc	ctg	tgc	agc	ctg	240

				_			_		•	,	T 1		^	0	1	
GIn 65	Leu	Ser	Ser	Pro	Ser 70	Arg	Pro	Ihr	GIN	Lys 75	Ihr	Leu	Cys	Ser	80	
					act Thr											288
					gac Asp											336
					agt Ser											384
ctg Leu	tgg Trp 130	tta Leu	gtg Val	tct Ser	tac Tyr	ctc Leu 135	att	ggc Gly	ttc Phe	ctc Leu	cca Pro 140	ctc Leu	gga Gly	atc Ile	ccc Pro	432
atg Met 145	ttc Phe	cag Gln	cag Gln	act Thr	gcc Ala 150	tac Tyr	aaa Lys	ggg Gly	cag Gln	tgc Cys 155	Ser	ttc Phe	ttt Phe	gct Ala	gta Val 160	480
			His		gtg Val			Leu								528
					gtc Val											576
tcc Ser	atg Met	cac His 195	agc Ser	cag Gln	cag Gln	att Ile	cga Arg 200	aag Lys	atg Met	gaa Glu	cat His	gca Ala 205	gga Gly	gcc Ala	atg Met	624
gct Ala	gga Gly 210	Gly	tat Tyr	cga Arg	tcc Ser	cca Pro 215	cgg Arg	act Thr	ccc Pro	agc Ser	gac Asp 220	Phe	aaa Lys	gct Ala	ctc Leu	672
cgt Arg 225	Thr	gtg Val	tct Ser	gtt Val	ctc Leu 230	He	ggg Gly	agc Ser	ttt Phe	gct Ala 235	Leu	tcc Ser	tgg Trp	acc Thr	ccc Pro 240	720
ttc Phe	ctt Leu	ato Ile	act Thr	ggc Gly 245	ile	gtg Val	cag Gln	gtg Val	gcc Ala 250	Cys	cag Gln	gag Glu	tgt Cys	cac His 255	ctc Leu	768

lyr					cgg Arg											816
					atc Ile											864
cag Gln	ctc Leu 290	tac Tyr	cac His	atg Met	gcc Ala	cta Leu 295	gga Gly	gtg Val	aag Lys	aag Lys	gtg Val 300	ctc Leu	acc Thr	tca Ser	ttc Phe	912
					gcc Ala 310											960
agt Ser	tcc Ser	tgt Cys	cac His	atc lle 325	gtc Val	act Thr	atc He	tcc Ser	agc Ser 330	tca Ser	gag Glu	ttt Phe	gat Asp	ggc Gly 335	taa	1008
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Met Phe (GIn Gin		Ala Tyr 150	Lys	Gly	GIn	Cys 155	Ser	Phe	Phe	Ala	Va I 160
Phe His F	Pro His	Phe V 165	/al Leu	Thr	Leu	Ser 170	Cys	Val	Gly	Phe	Phe 175	Pro
Ala Met l	Leu Leu 180		/al Phe	Phe	Tyr 185	Cys	Asp	Met	Leu	Lys 190	lle	Ala
Ser Met h		GIn G	Gin lle	Arg 200	Lys	Met	Glu	His	Ala 205	Gly	Ala	Met
Ala Gly (210	Gly Tyr	Arg S	Ser Pro 215	Arg	Thr	Pro	Ser	Asp 220	Phe	Lys	Ala	Leu
Arg Thr \ 225	Val Ser		_eu lle 230	Gly	Ser	Phe	Ala 235	Leu	Ser	Trp	Thr	Pro 240
Phe Leu	lle Thr	Gly 1 245	lle Val	Gln	Val	Ala 250	Cys	GIn	Glu	Cys	His 255	Leu
Tyr Leu \	Va [°] l Leu 260		Arg Tyr	Leu	Trp 265	Leu	Leu	Gly	Val	Gly 270	Asn	Ser
Leu Leu /		Leu i	lle Tyr	Ala 280	Tyr	Trp	GIn	Lys	Glu 285	Val	Arg	Leu
GIn Leu 290		Met A	Ala Leu 295	Gly	Val	Lys	Lys	Val 300	Leu	Thr	Ser	Phe
Leu Leu I 305	Phe Leu		Ala Arg 310	Asn	Cys	Gly	Pro 315	Glu	Arg	Pro	Arg	Glu 320
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10
15

ctt atc att gct gtt aat gcg ctg gtg gtt gtg gct atg ctg cta tca 96 Leu lle lle Ala Val Asn Ala Leu Val Val Val Ala Met Leu Leu Ser 20 25 30

atc tac aag aat gat ggt gtt ggc ctt tgc ttc acc tta aat ctg gcc 144 lie Tyr Lys Asn Asp Gly Val Gly Leu Cys Phe Thr Leu Asn Leu Ala

		35					40					40				
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cag GIn 65	ctc Leu	tcc Ser	agc Ser	tct Ser	gct Ala 70	cag GIn	cac His	aca Thr	cag Gln	aag Lys 75	acc Thr	ttg [.] Leu	tgt Cys	agc Ser	ctt Leu 80	240
cgg Arg	atg Met	gca Ala	ttc Phe	gtc Val 85	act Thr	tct Ser	tct Ser	gca Ala	gcc Ala 90	gcc Ala	tct Ser	gtc Val	ctc Leu	acg Thr 95	gtc Val	288
atg Met	ctg Leu	att He	gcc Ala 100	ttt Phe	gac Asp	agg Arg	tac Tyr	ctg Leu 105	gcc Ala	att Ile	aag Lys	cag Gln	ccc Pro 110	ctc Leu	cgt Arg	336
tac Tyr	ttc Phe	cag Gln 115	atc e	atg Met	aat Asn	ggg Gly	ctt Leu 120	gta Val	gcc Ala	gga Gly	gga Gly	tgc Cys 125	att He	gca Ala	ggg Gly	384
ctg Leu	tgg Trp 130	ttg Leu	ata Ile	tct Ser	tac Tyr	ctt Leu 135	atc Ile	ggc Gly	ttc Phe	ctc Leu	cca Pro 140	ctt Leu	gga Gly	gtc Val	tcc Ser	432
ata Ile 145	ttc Phe	cag Gln	cag Gln	acc Thr	acc Thr 150	tac Tyr	cat His	ggg Gly	ccc Pro	tgc Cys 155	acc Thr	ttc Phe	ttt Phe	gct Ala	gtg Val 160	480
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gct Ala	gtg Val	ctc Leu	ctc Leu 180	ttt Phe	gtc Val	ttc Phe	ttc Phe	tac Tyr 185	tgt Cys	gac Asp	atg Met	ctc Leu	aag Lys 190	att e	gcc Ala	576
tct Ser	gtg Val	cac His 195	Ser	cag GIn	cac His	atc Ile	cgg Arg 200	aag Lys	atg Met	gaa Glu	cat His	gca Ala 205	Gly	gcc Ala	atg Met	624
gtt Val	gga Gly 210	Ala	tgc Cys	cgg Arg	ccc Pro	cca Pro 215	Arg	cct Pro	gtc Val	aat Asn	gac Asp 220	Phe	aag Lys	gct Ala	gtc Val	672

cgg Arg 225	act Thr	gta Val	tct Ser	gtc Val	ctt Leu 230	att He	ggg Gly	agc Ser	ttc Phe	acc Thr 235	ctg Leu	tcc Ser	tgg Trp	tct Ser	ccg Pro 240	720
ttt Phe	ctc Leu	atc Ile	act Thr	agc Ser 245	att Ile	gtg Val	cag GIn	gtg Val	gcc Ala 250	tgc Cys	cac His	aaa Lys	tgc Cys	tgc Cys 255	ctc Leu	768
tac Tyr	caa Gln	gtg Val	ctg Leu 260	gaa Glu	aaa Lys	tac Tyr	ctc Leu	tgg Trp 265	ctc Leu	ctt Leu	gga Gly	gtt Val	ggc Gly 270	aac Asn	tcc Ser	816
ctg Leu	ctc Leu	aac Asn 275	cca Pro	ctc Leu	atc Ile	tat Tyr	gcc Ala 280	tat Tyr	tgg Trp	cag Gln	agg Arg	gag Glu 285	gtt Val	cgg Arg	cag GIn	864
cag Gln	ctc Leu 290	tgc Cys	cac His	atg Met	gcc Ala	ctg Leu 295	ggg Gly	gtg Val	aag Lys	aag Lys	ttc Phe 300	ttt Phe	act Thr	tca Ser	atc Ile	912
				tcg Ser												960
agc Ser	tcc Ser	tat Tyr	cac His	atc Ile 325	gtc Val	act Thr	atc Ile	agc Ser	cag Gln 330	ccg Pro	gag Glu	ctc Leu	gat Asp	ggc Gly 335	tag	1008
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1			Ala	5 Val				Val	10 Val				Leu	15 Leu	Ser	
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Val	Ala 50			Leu	lle	Gly 55			He	Ser	Gly 60	Leu		Thr	Asp	
GIr 65	l Leu		Ser	Ser	A1a 70	Gln		Thr	Gln	Lys 75	Thr		Cys	Ser	Leu 80	
		: Ala	Phe	· Val			Ser	Ala	Ala			Val	Leu	Thr	Val	

				85					90					95	
			100					105					Pro 110		
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Leu	Trp 130		lle	Ser	Tyr	Leu 135	He	Gly	Phe	Leu	Pro 140	Leu	Gly	Val	Ser
11e 145	Phe	GIn	Gln	Thr	Thr 150	Tyr		Gly	Pro	Cys 155	Thr		Phe	Ala	Va I 160
Phe	His	Pro	Arg	Phe 165	Val	Leu	Thr	Leu	Ser 170	Cys	Ala	Gly	Phe	Phe 175	Pro
Ala	Val	Leu	Leu 180		Val	Phe	Phe	Tyr 185	Cys	Asp	Met	Leu	Lys 190	lle	Ala
Ser	Val	His 195	Ser	Gln	His	He	Arg 200	Lys	Met	Glu	His	Ala 205	Gly	Ala	Met
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Phe	Leu	He	Thr	Ser 245	He		Gin	Val	Ala 250	Cys	His	Lys	Cys	Cys 255	Leu
Tyr	Glņ	Val	Leu 260	Glu	Lys	Tyr	Leu	Trp 265	Leu	Leu	Gly	Val	Gly 270	Asn	Ser
Leu	Leu	Asn 275	Pro	Leu	He	Tyr	Ala 280		Trp	Gln	Arg	Glu 285	Val	Arg	Gln
Gin	Leu 290	Cys	His	Met	Ala	Leu 295	Gly	Val	Lys	Lys	Phe 300	Phe	Thr	Ser	lle
Phe 305	Leu		Leu	Ser	Ala 310		Asn	Arg	Gly	Pro 315	Gln	Arg	Thr	Arg	Glu 320
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<212> DNA

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<220>

Obscription of Artificial Sequence: an artificially synthesized primer sequence

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<213>	Arti	ficial Sequ	ienće				
<220>							Virtillag_
<223>		cription of mer sequence	Artificial	Sequence: a	an artificia	ally synthe	esized
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cacagad	cca	gcaccaggga	aatggtccgg	aaattgcagc	ctcagccccc	agccatctgo	240
cgaccc	ccc	accccaggcc	ctaatgggcc	aggcggcagg	ggttgacagg	taggggagat	300
gggctct	gag	actataaagc	cagcgggggc	ccagcagccc	tcagccctcc	aggacaggc	t 360
gcatcag	gaag	aggccat					377